



TITLE: NEW RECEPTOR AND RELATED PRODUCTS AND METHODS #4  
INVENTORS NAME: Byoung S. Kwon  
SERIAL NO.: 10/027,199

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ATGTCCATGA	ACTGCTGAGT	GGATAAACAG	CACGGGATAT	CTCTGTCTAA	-96
AGGAATATTA	CTACACCAGG	AAAAGGACAC	ATTTCGACAAC	AGGAAAGGAG	-46
CCTGTCACAG	AAAACCACAG	TGTCCTGTGC	ATGTGACATT	TCGCC	-1
ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA	45				
<u>Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu</u>					
GTG GGC TGT GAG AAG GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC	90				
<u>Val Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn</u>					
TGT CAG CCT GGT ACT TTC TGC AGA AAA TAC AAT CCA GTC TGC AAG	135				
<u>Cys Gln Pro Gly Thr Phe Cys Arg Lys Tyr Asn</u>					
AGC TGC CCT CCA AGT ACC TTC TCC AGC ATA GGT GGA CAG CCG AAC	180				
<u>Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn</u>					
TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG	225				
<u>Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys</u>					
TTT TGC TCC TCT ACC CAC AAC GCG GAG TGT GAG TGC ATT GAA GGA	270				
<u>Phe Cys Ser Ser Thr His Asn Ala Glu Cys Glu Cys Ile Glu Gly</u>					
TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA TGT GAA AAG GAC TGC	315				
<u>Phe His Cys Leu Gly Pro Gln Cys Thr Arg Cys Glu Lys Asp Cys</u>					
AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC	360				
<u>Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser</u>					
TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC	405				
<u>Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro</u>					
TGG ACG AAC TGC TCT CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG	450				
<u>Trp Thr Asn Cys Ser Leu Asp Gly Arg Ser Val Leu Lys Thr Gly</u>					
ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC CCT GTG GTG AGC TTC	495				
<u>Thr Thr Glu Lys Asp Val Val Cys Gly Pro Pro Val Val Ser Phe</u>					
TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA	540				
<u>Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly</u>					
GGG CAC TCC TTG CAG GTC ACC TTG TTC CTG GCG CTG ACA TCG	585				
<u>Gly His Ser Leu Glu Val Leu Thr Leu Phe Leu Ala Leu Thr Ser</u>					
GCT TTG CTG CTG GCC CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG	630				
<u>Ala Leu Leu Leu Ala Leu Ile Phe Ile Thr Leu Leu Phe Ser Val</u>					

Fig. 1

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CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC ATA TTC AAG CAA CCA	675
<u>Leu</u> Lys Trp Ile Arg Lys Lys Phe Pro His Ile Phe Lys Gln Pro	
TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC	720
Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser	
TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGA GGC TAT GAG	765
Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu	
CTG TGA	771
Leu ---	
TGTACTATCC TAGGAGATGT GTGGGCCGAA ACCGAGAAGC ACTAGGACCC	821
CACCATCCTG TGGAAACAGCA CAAGCAACCC CACCACCCTG TTCTTACACA	871
TCATCCTAGA TGATGTGTGG GCGCGCACCT CATCCAAGTC TCTTCTAACG	921
CTAACATAT TGTCTTTACC TTTTAAAAAT CTTTAAAAAT	971
TATGTGTGTG AGTGTTTTGC CTGCCTGTAT GCACACGTGT GTGTGTGTGT	1021
GTGTGTGACA CTCCTGATGC CTGAGGAGGT CAGAAGACAA AGGGTTGGTT	1071
CCATAAGAAC TGGAGTTATG GATGGCTGTG AGCCGGNNNG ATAGGTGCGG	1121
ACGGAGACCT GTCTTCTTAT TTTAACGTGA CTGTATAATA AAAAAAAAAAT	1171
GATATTTTCG GAATTGTAGA GATTGTCTGT ACACCCCTCT AGTTAATGAT	1221
CTAAGAGGAA TTGTTGATAC GTAGTATACT GTATATGTGT ATGTATATGT	1271
ATATGTATAT ATAAGACTCT TTTACTGTCA AAGTCAACCT AGAGTGTCTG	1321
GTTACCAGGT CAATTTTATT GGACATTTTA CGTCACACAC ACACACACAC	1371
ACACACACAC ACGTTTATAC TACGTACTGT TATCGGTATT CTACGTCATA	1421
TAATGGGATA GGGTAAAAGG AAACCAAAGA GTGAGTGATA TTATTGTGGA	1471
GGTGACAGAC TACCCCTTCT GGTACGTTAG GGACAGACCT CCTTCGGACT	1521
GTCTAAAACT CCCCTTAGAA GTCTCGTCAA GTTCCCGGAC GAAGAGGACA	1571
GAGGAGACAC AGTCCGAAAA GTTATTTTTC CGGCAAAATCC TTTCCCTGTT	1621
TCGTGACACT CCACCCCTTG TGGACACTTG AGTGTCTATCC TTGCGCCGGA	1671
AGGTGAGGTG GTACCCGTCT GTAGGGGCGG GGAGACAGAG CCGCGGGGGA	1721
GCTACAGGAA TCGACTCACA GGGCGCCCCG GGCTTCGCAA ATGAAACTTT	1771
TTTAATCTCA CAAGTTTCGT CCGGGCTCGG CGGACCTATG GCGTCGATCC	1821
TTATTACCTT ATCCTGGCGC CAAGATAAAA CAACCAAAAG CCTTGACTCC	1871
GGTACTAATT CTCCCCTGCC GCCCCCGTAA GCATAACGCG GCGATCTCCA	1921
CTTTAAGAAC CTGGCCGCGT TCTGCCTGGT CTCGCTTTCG TAAACCGTTC	1971
TTACAAAAGT AATTAGTTCT TGCTTTTCAG CTCCAAGCTT CTGCTAGTCT	2021
ATGGCAGCAT CAAGGCTGGT ATTTGCTACG GCTGACCGCT ACGCCGCGCG	2071
AATAAGGGTA CTGGGCGGCC CGTCGAAGGC CCTTTGGTTT CAGAAACCCA	2121
AGGCCCCCTC CATACCAACG TTTTCGACTTT GATTCTTGCC GGTACGTGGT	2171
GGTGGGTGCC TTAGCTCTTT CTGCATAGTT AGAC	2205

*Fig. 1 Cont'd*

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human homologue of mouse 4-1bb

h4-1bb Length 838

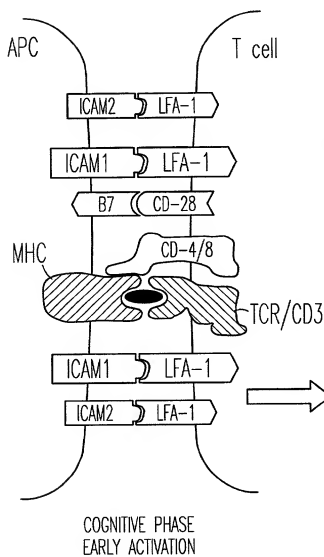
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101	ACAAGATCAT	TGCAGGATCC	TTGTAGTAAC	TGCCCAGCTG	GTACATTCTG
151	TGATAATAAC	AGGAATCAGA	TTTGCACTCC	CTGTCTCCA	AATAGTTTCT
201	CCAGCGCAGG	TGGACAAAGG	ACCTGTGACA	TATGCAGGCA	GTGTAAGGT
251	GTTTTTCAGGA	CCAGGAAGGA	GTGTTCTCTC	ACCAGCAATG	CAGAGTGTGA
301	CTGCACTCCA	GGGTTTCACT	GCCTGGGGGC	AGGATGCAGC	ATGTGTGAAC
351	AGGATTGTAA	ACAAGGTCAA	GAACTGACAA	AAAAAGGTTG	TAAAGACTGT
401	TGCTTTGGGA	CATTTAACGA	TCAGAAACGT	GGCATCTGTC	GACCTGGAC
451	AAACTGTTCT	TTGGATGGAA	AGTCTGTGCT	TGTGAATGGG	ACGAAGCAGA
501	GGGACGTGGT	CTGTGGACCA	TCTCCAGCTG	ACCTCTCTCC	GGGAGCATCC
551	TCTGTGACCC	CGCTGCCCC	TGCGAGAGAG	CCAGGACACT	CTCCGCAGAT
601	CATCTCCTTC	TTTTTTGCGC	TGACGTCGAC	TGCGTTGCTC	TTCTGTCTGT
651	TCTTCCTCAC	GCTCCGTTTC	TCTGTTGTTA	AACGGGGCAG	AAAGAACTC
701	CTGTATATAT	TCAAACAACC	ATTTATGAGA	CCAGTACAAA	CTACTCAAGA
751	GGAAAGATGGC	TGTAGCTGCC	GATTCCAGA	AGAAGAAGAA	GGAGGATGTG
801	AACGTGTGAAA	TGGAAGTCAA	TAGGGCTGTT	GGGACTTT	

*Fig. 2A*

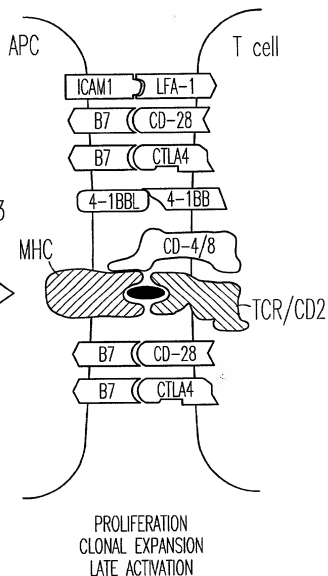
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101	MCEQDCKQGQ	ELTKKGCKDC	CFGTFNDQKR	GICRPWTNCS	LDGKSVLVNG
151	TKERDVVCGP	SPADLSPGAS	SVTPPAPARE	PGHSPQIISF	FLALTSTALL
201	FLFFFLTLRF	SVVKRGRKKL	LYIFKQPFMR	PVQTTQEEDG	CSCRFPEEEE
251	GGCEL				

*Fig. 2B*

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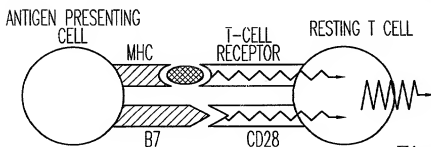


*Fig. 3a*

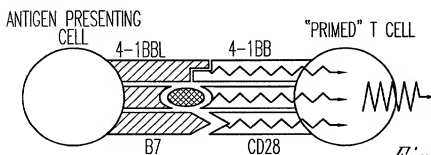


*Fig. 3b*

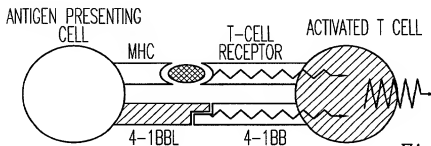
NORMAL T CELL ACTIVATION PATHWAY



*Fig. 4a*



*Fig. 4b*



*Fig. 4c*

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BLOCKING STEPS IN T-CELL ACTIVATION PATHWAY

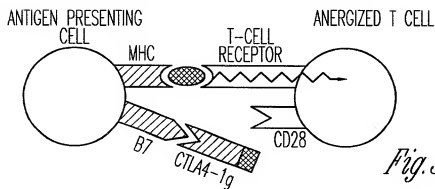


Fig. 5a

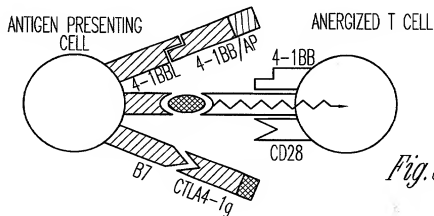


Fig. 5b

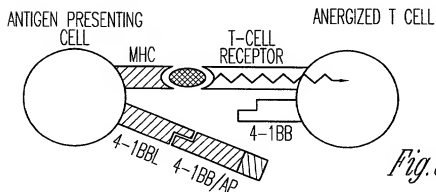


Fig. 5c